

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/559,434A  
Source: IFWJO  
Date Processed by STIC: 5/19/06

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 05/19/2006

PATENT APPLICATION: US/10/559,434A

TIME: 12:04:23

Input Set : A:\May.ST25.txt

Output Set: N:\CRF4\05192006\J559434A.raw

3 <110> APPLICANT: Degussa AG  
 4 May, Oliver  
 5 Drauz, Karlheinz  
 6 Buchholz, Stefan  
 8 <120> TITLE OF INVENTION: Screening Process for Hydantoin Racemases  
 10 <130> FILE REFERENCE: 7601/84454  
 12 <140> CURRENT APPLICATION NUMBER: 10/559,434A  
 13 <141> CURRENT FILING DATE: 2005-12-05  
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/005239  
 16 <151> PRIOR FILING DATE: 2004-05-15  
 18 <160> NUMBER OF SEQ ID NOS: 16  
 20 <170> SOFTWARE: PatentIn version 3.3  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 6  
 24 <212> TYPE: PRT  
 25 <213> ORGANISM: Artificial sequence  
 27 <220> FEATURE:  
 28 <223> OTHER INFORMATION: consensus sequence found in hydantoin racemase sequence of  
 29 Arthrobacter crystallopoietes  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: misc\_feature  
 34 <222> LOCATION: (2)..(2)  
 35 <223> OTHER INFORMATION: Xaa is an amino acid selected from A, R, N, D, C, Q, E, H, I,  
 L,  
 36 K, M, F, P, S, T, Y or V  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: misc\_feature  
 40 <222> LOCATION: (4)..(4)  
 41 <223> OTHER INFORMATION: Xaa is an amino acid selected from P and T  
 43 <400> SEQUENCE: 1  
 W--> 45 Phe Xaa Asp Xaa Gly Leu  
 46 1 5  
 49 <210> SEQ ID NO: 2  
 50 <211> LENGTH: 236  
 51 <212> TYPE: PRT  
 52 <213> ORGANISM: Arthrobacter crystallopoietes  
 54 <400> SEQUENCE: 2  
 56 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu  
 57 1 5 10 15  
 60 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile  
 61 20 25 30  
 64 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe  
 65 35 40 45  
 68 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala

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69      50      55      60
72 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Gly Asp
73 65      70      75      80
76 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
77      85      90      95
80 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
81      100      105      110
84 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
85      115      120      125
88 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
89      130      135      140
92 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
93 145      150      155      160
96 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
97      165      170      175
100 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
101      180      185      190
104 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
105      195      200      205
108 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
109      210      215      220
112 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
113 225      230      235
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117 <211> LENGTH: 711
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: mutated hydantoin racemase sequence of Arthrobacter
123      crystallopoietes
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128 gcagcacaac aagttgtcgc gaccggcacc ataatttctg ccatcaaccc ctccagagga      120
130 cccgccgtca ttgaaggcag ctttgacgaa gcactggcca cgttccatct cattgaagag      180
132 gtggagcgcg ctgagcggga aaacccgccc gacgcctacg tcatcgcatg tttcagggat      240
134 ccgggacttg acgcggtcaa ggagctgact gacaggccag tggtaggagt tgccgaagct      300
136 gcaatccaca tgtcttcatt cgtcgcggcc accttctcca ttgtcagcat cctcccgagg      360
138 gtcaggaaac atctgcacga actggtacgg caagcggggg cgacgaatcg cctcgctcc      420
140 atcaagctcc caaatctggg ggtgatggcc ttccatgagg acgaacatgc cgactggag      480
142 acgctcaaac aagccgcaa ggaggcggtc caggaggacg gcgccgagtc gatagtgtc      540
144 ggatgcgccg gcatggtggg gtttgcgctg caactgagcg acgaactcgg cgtccctgtc      600
146 atcgaccccg tcgaggcagc ttgccgcgtg gccgagagtt tggtcgctct gggctaccag      660
148 accagcaaag cgaactcgta tcaaaaaccg acagagaagc agtacctcta g      711
151 <210> SEQ ID NO: 4
152 <211> LENGTH: 236
153 <212> TYPE: PRT
154 <213> ORGANISM: Artificial sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: mutated hydantoin racemase sequence of Arthrobacter

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158      crystallopoietes
160 <400> SEQUENCE: 4
162 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
163 1      5      10      15
166 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
167      20      25      30
170 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
171      35      40      45
174 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala
175      50      55      60
178 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Arg Asp
179 65      70      75      80
182 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
183      85      90      95
186 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
187      100     105     110
190 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
191      115     120     125
194 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
195      130     135     140
198 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
199 145     150     155     160
202 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
203      165     170     175
206 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
207      180     185     190
210 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
211      195     200     205
214 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
215      210     215     220
218 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
219 225     230     235
222 <210> SEQ ID NO: 5
223 <211> LENGTH: 711
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: mutated hydantoin racemase sequence of Arthrobacter
229      crystallopoietes
231 <400> SEQUENCE: 5
232 atgagaatcc tcgtgatcaa cccaacagt tccagcgccc ttactgaatc ggttgcgagc      60
234 gcagcacaac aagttgtcgc gaccggcacc ataatttctg ccatcaaccc ctccagagga      120
236 cccgccgtca ttgaaggcag ctttgacgaa gcactggcca cgttccatct cattgaagag      180
238 ctggagcgcg ctgagcggga aaaccgcgcc gacgcctacg tcatcgcatg tttcgaggat      240
240 cggggacttg acgcggtcaa ggagctgact gacaggccag tggtaggagt tgccgaagct      300
242 gcaatccaca tgtcttcatt cgctcgcgcc accttctcca ttgtcagcat cctcccagg      360
244 gtcaggaaac atctgcacga actggtacgg caagcggggg cgacgaatcg cctcgctcc      420
246 atcaagctcc caaatctggg ggtgatggcc ttccatgagg acgaacatgc cgcactggag      480
248 acgctcaaac aagccgcca ggaggcggtc caggaggacg gcgccgagtc gatagtgtc      540

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250 ggatgcgccg gcattggtggg gtttgcgcgt caactgagcg acgaactcgg cgtccctgtc      600
252 atcgaccccg tcgaggcagc ttgccgcgtg gccgagagtt tggtcgctct gggctaccag      660
254 accagcaaag cgaactcgta tcaaaaaccg acagagaagc agtacctcta g                711
257 <210> SEQ ID NO: 6
258 <211> LENGTH: 236
259 <212> TYPE: PRT
260 <213> ORGANISM: Artificial sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: mutated hydantoin racemase sequence of Arthrobacter
264     crystallopoietes
266 <400> SEQUENCE: 6
268 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
269 1           5           10           15
272 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
273           20           25           30
276 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
277           35           40           45
280 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala
281           50           55           60
284 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Glu Asp
285 65           70           75           80
288 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
289           85           90           95
292 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
293           100          105          110
296 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
297           115          120          125
300 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
301           130          135          140
304 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
305 145          150          155          160
308 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
309           165          170          175
312 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
313           180          185          190
316 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
317           195          200          205
320 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
321           210          215          220
324 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
325 225          230          235
328 <210> SEQ ID NO: 7
329 <211> LENGTH: 711
330 <212> TYPE: DNA
331 <213> ORGANISM: Artificial sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: mutated hydantoin racemase sequence of Arthrobacter
335     crystallopoietes
337 <400> SEQUENCE: 7

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338 atgagaatcc tcgtgatcaa ccccaacagt tccagcgccc ttactgaatc ggttgccggac      60
340 gcagcacaaac aagttgtcgc gaccggcacc ataatttctg ccatcaaccc ctccagagga      120
342 cccgccgtca ttgaaggcag ctttgacgaa gcaactggcca cgttccatct cattgaagag      180
344 gtggagcgcg ctgagcggga aaacccgccc gacgcctacg tcacgcgatg tttccaggat      240
346 ccgggacttg acgcggtcaa ggagctgact gacaggccag tggtaggagt tgccgaagct      300
348 gcaatccaca tgtcttcatt cgtcgcggcc accttctcca ttgtcagcat cctcccgagg      360
350 gtcaggaaac atctgcacga actggtagcg caagcggggg cgacgaatcg cctcgcctcc      420
352 atcaagctcc caaatctggg ggtgatggcc ttccatgagg acgaacatgc cgcactggag      480
354 acgctcaaac aagccgccaa ggaggcggtc caggaggacg gcgccgagtc gatagtgtct      540
356 ggatgcgcgc gcatgggtgg gtttgcgctg caactgagcg acgaactcgg cgtccctgtc      600
358 atcgaccccg tcgaggcagc ttgccgcgtg gccgagagtt tggtcgctct gggctaccag      660
360 accagcaaag cgaactcgta tcaaaaaccg acagagaagc agtacctcta g              711
363 <210> SEQ ID NO: 8
364 <211> LENGTH: 236
365 <212> TYPE: PRT
366 <213> ORGANISM: Artificial sequence
368 <220> FEATURE:
369 <223> OTHER INFORMATION: mutated hydantoin racemase sequence of Arthrobacter
370     crystallopoietes
372 <400> SEQUENCE: 8
374 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
375 1          5          10          15
378 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
379          20          25          30
382 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
383          35          40          45
386 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala
387          50          55          60
390 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Gln Asp
391 65          70          75          80
394 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
395          85          90          95
398 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
399          100         105         110
402 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
403          115         120         125
406 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
407          130         135         140
410 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
411 145         150         155         160
414 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
415          165         170         175
418 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
419          180         185         190
422 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
423          195         200         205
426 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
427          210         215         220
430 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 05/19/2006  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,4  
Seq#:14; N Pos. 49

VERIFICATION SUMMARY

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L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0